

Appendix II: Alignment of the CMV IE promoter sequence of M60321 and instant SEQ ID NO: 3

BLASTN 2.2.25+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: N062GZNX111

Query= gi|330624|gb|M60321.1|HS5MIEP Human cytomegalovirus major immediate-early protein gene, 5' end

Length=2361

Sequences producing significant alignments:	Score (Bits)	E Value
lcl 54011 SID_3	115	3e-30

ALIGNMENTS

>lcl|54011 SID_3

Length=3584

Score = 115 bits (62), Expect = 3e-30
 Identities = 62/62 (100%), Gaps = 0/62 (0%)
 Strand=Plus/Plus

Query	1082	CAAAATGGGCGGTAGGCGGTGTACGGTGGGAGGTC	TATATAAGCAGAGCTCGTTTAGTGAAC	1141
Sbjct	577	CAAAATGGGCGGTAGGCGGTGTACGGTGGGAGGTC	TATATAAGCAGAGCTCGTTTAGTGAAC	636
Query	1142	CG	1143	
Sbjct	637	CG	638	